



ENTERED

TIME: 11:00:45

Output Set: N:\CRF3\02262002\I602833B.raw

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MAR 14 2002  
TECH CENTER 1600/2900

## RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/09/602,833B

TIME: 11:00:45

Input Set : A:\8535036999.txt

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59	115	120	125	
61	agc aat acc ttg att caa atc att cct aca tat att cag tta ttt caa	432		
62	Ser Asn Thr Leu Ile Gln Ile Ile Pro Thr Tyr Ile Gln Leu Phe Gln			
63	130	135	140	
65	gcg atg aga att ctg gat ctg cca aaa aac caa atc tca cat ctt cca	480		
66	Ala Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro			
67	145	150	155	160
69	gca gaa atc ggt tgt ttg aag aac ctg aaa gaa ctc aat gtg ggt ttc	528		
70	Ala Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe			
71	165	170	175	
73	aac tat ctg aag agc att cct cca gaa ttg gga gat tgt gaa aat cta	576		
74	Asn Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu			
75	180	185	190	
77	gag aga ctg gat tgt tct gga aat cta gaa tta atg gag ctg ccc ttt	624		
78	Glu Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe			
79	195	200	205	
81	gaa tta agt aat ttg aag caa gtt aca ttt gta gat atc tca gca aac	672		
82	Glu Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn			
83	210	215	220	
85	aag ttt tcc agt gtc cca atc tgt gtc ctg cgg atg tgc aat ttg cag	720		
86	Lys Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln			
87	225	230	235	240
89	tgg ttg gat atc agc agc aat aac ctg acc gac ctg ccg caa gat ata	768		
90	Trp Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile			
91	245	250	255	
93	gac agg cta gag gag ctg cag agc ttt ctc ttg tat aaa aac aag ttg	816		
94	Asp Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu			
95	260	265	270	
97	acc tac ctt ccc tat tcc atg ctg aac ctg aag aag ctc act ctg tta	864		
98	Thr Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu			
99	275	280	285	
101	gtc gtc agt ggg gac cat ttg gtg gag ctc cca act gcc ctt tgt gac	912		
102	Val Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp			
103	290	295	300	
105	tca tcc aca cct tta aaa ttt gta agc ctt atg gac aat cct att gat	960		
106	Ser Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp			
107	305	310	315	320
109	aat gcc caa tgt gaa gat ggc aat gaa ata atg gaa agt gaa cgg gat	1008		
110	Asn Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp			
111	325	330	335	
113	cgc caa cat ttt gat aaa gaa gtt atg aaa gcc tat att gaa gac ctt	1056		
114	Arg Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu			
115	340	345	350	
117	aaa gaa aga gaa tct gtt ccc agc tat acc acc aaa gtg tct ttt agc	1104		
118	Lys Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser			
119	355	360	365	
121	ctt caa ctt tga	1116		
122	Leu Gln Leu			
123	370			

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```

126 <210> SEQ ID NO: 2
127 <211> LENGTH: 371
128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapien
131 <400> SEQUENCE: 2
132 Met Gly His Lys Val Val Val Phe Asp Ile Ser Val Ile Arg Ala Leu
133   1          5          10          15
134 Trp Glu Thr Arg Val Lys Lys His Lys Ala Trp Gln Lys Lys Glu Val
135          20          25          30
136 Glu Arg Leu Glu Lys Ser Ala Leu Glu Lys Ile Lys Glu Glu Trp Asn
137          35          40          45
138 Phe Val Ala Glu Cys Arg Arg Lys Gly Ile Pro Gln Ala Val Tyr Cys
139          50          55          60
140 Lys Asn Gly Phe Ile Asp Thr Ser Val Arg Leu Asp Lys Ile Glu
141          65          70          75          80
142 Arg Asn Thr Leu Thr Arg Gln Ser Ser Leu Pro Lys Asp Arg Gly Lys
143          85          90          95
144 Arg Ser Ser Ala Phe Val Phe Glu Leu Ser Gly Glu His Trp Thr Glu
145          100         105         110
146 Leu Pro Asp Ser Leu Lys Glu Gln Thr His Leu Arg Glu Trp Tyr Ile
147          115         120         125
148 Ser Asn Thr Leu Ile Gln Ile Ile Pro Thr Tyr Ile Gln Leu Phe Gln
149          130         135         140
150 Ala Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro
151          145         150         155         160
152 Ala Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe
153          165         170         175
154 Asn Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu
155          180         185         190
156 Glu Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe
157          195         200         205
158 Glu Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn
159          210         215         220
160 Lys Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln
161          225         230         235         240
162 Trp Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile
163          245         250         255
164 Asp Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu
165          260         265         270
166 Thr Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu
167          275         280         285
168 Val Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp
169          290         295         300
170 Ser Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp
171          305         310         315         320
172 Asn Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp
173          325         330         335
174 Arg Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu
175          340         345         350

```

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```

176  Lys Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser
177          355                      360                      365
178  Leu Gln Leu
179          370
181 <210> SEQ ID NO: 3
182 <211> LENGTH: 681
183 <212> TYPE: DNA
184 <213> ORGANISM: Homo sapien
186 <220> FEATURE:
187 <221> NAME/KEY: CDS
188 <222> LOCATION: (1)...(678)
190 <400> SEQUENCE: 3
191  atg aga att ctg gat ctg cca aaa aac caa atc tca cat ctt cca gca      48
192  Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro Ala
193    1          5          10          15
195  gaa atc ggt tgt ttg aag aac ctg aaa gaa ctc aat gtg ggt ttc aac      96
196  Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe Asn
197          20          25          30
199  tat ctg aag agc att cct cca gaa ttg gga gat tgt gaa aat cta gag      144
200  Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu Glu
201          35          40          45
203  aga ctg gat tgt tct gga aat cta gaa tta atg gag ctg ccc ttt gaa      192
204  Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe Glu
205          50          55          60
207  tta agt aat ttg aag caa gtt aca ttt gta gat atc tca gca aac aag      240
208  Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn Lys
209    65          70          75          80
211  ttt tcc agt gtc cca atc tgt gtc ctg cgg atg tcg aat ttg cag tgg      288
212  Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln Trp
213          85          90          95
215  ttg gat atc agc agc aat aac ctg acc gac ctg ccg caa gat ata gac      336
216  Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile Asp
217          100          105          110
219  agg cta gag gag ctg cag agc ttt ctc ttg tat aaa aac aag ttg acc      384
220  Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu Thr
221          115          120          125
223  tac ctt ccc tat tcc atg ctg aac ctg aag aag ctc act ctg tta gtc      432
224  Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu Val
225          130          135          140
227  gtc agt ggg gac cat ttg gtg gag ctc cca act gcc ctt tgt gac tca      480
228  Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp Ser
229    145          150          155          160
231  tcc aca cct tta aaa ttt gta agc ctt atg gac aat cct att gat aat      528
232  Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp Asn
233          165          170          175
235  gcc caa tgt gaa gat ggc aat gaa ata atg gaa agt gaa cgg gat cgc      576
236  Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp Arg
237          180          185          190
239  caa cat ttt gat aaa gaa gtt atg aaa gcc tat att gaa gac ctt aaa      624

```

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```

240  Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu Lys
241      195                      200                      205
243  gaa aga gaa tct gtt ccc agc tat acc acc aaa gtg tct ttt agc ctt      672
244  Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser Leu
245      210                      215                      220
247  caa ctt tga      681
248  Gln Leu
249  225
252 <210> SEQ ID NO: 4
253 <211> LENGTH: 226
254 <212> TYPE: PRT
255 <213> ORGANISM: Homo sapien
257 <400> SEQUENCE: 4
258  Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro Ala
259      1                      5                      10                      15
260  Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe Asn
261      20                      25                      30
262  Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu Glu
263      35                      40                      45
264  Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe Glu
265      50                      55                      60
266  Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn Lys
267      65                      70                      75                      80
268  Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln Trp
269      85                      90                      95
270  Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile Asp
271      100                     105                     110
272  Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu Thr
273      115                     120                     125
274  Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu Val
275      130                     135                     140
276  Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp Ser
277      145                     150                     155                     160
278  Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp Asn
279      165                     170                     175
280  Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp Arg
281      180                     185                     190
282  Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu Lys
283      195                     200                     205
284  Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser Leu
285      210                     215                     220
286  Gln Leu
287  225

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VERIFICATION SUMMARY

DATE: 02/26/2002

PATENT APPLICATION: US/09/602,833B

TIME: 11:00:46

Input Set : A:\8535036999.txt

Output Set: N:\CRF3\02262002\I602833B.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

STIC-Biot ch/Ch mLib

60672

From: Chan, Christina  
Sent: Wednesday, February 20, 2002 1:52 PM  
To: Li, Janice; STIC-Biotech/ChemLib  
Subject: RE: 09/602,833

Please rush. Thanks Chris

-----Original Message-----

From: Li, Janice  
Sent: Wednesday, February 20, 2002 1:48 PM  
To: Chan, Christina  
Subject: 09/602,833

Hi, Chris:

Could you please give approval for rush search SEQ ID Nos: 1 and 3 of US 09/602,833 against all commercial databases including pending patent database.

Please print results containing sequences having >24 contiguous bases of SEQ ID Nos: 1 or 3.

This is an amended case.

Thanks

STIC-Biotech/ChemLib

Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

From: Spencer, Mark  
Sent: Friday, February 22, 2002 9:31 AM  
To: Li, Janice; STIC-Biotech/ChemLib  
Subject: RE: 09/602,833

Janice,  
When I checked the ABSS system there were sequences entered for this case. So, I updated PALM with a CRFE. The sequences can be searched at anytime.

Thanks,  
Mark

-----Original Message-----

From: Li, Janice  
Sent: Wednesday, February 20, 2002 2:43 PM  
To: STIC-Biotech/ChemLib  
Cc: Spencer, Mark  
Subject: RE: 09/602,833

The corrected CRF just entered today. The paper record indicates that raw listing has been entered, no error report was given. Are you looking at this updated record? If that is the case, could you give an error report, so I can communicate with the applicants?

Thanks for your attention.

Janice

pending / resumed

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 2/25/02  
Date Completed: 2/26/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: 4  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST(where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: 05  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_